

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Leu	Phe	Val	Gln	Asp	Tyr	Leu	Leu	Pro	Thr	Cys	Ile	Pro
1				5					10			

### Claims

1. A transcriptional activator comprising:  
a DNA binding moiety; and  
a peptide approximately 6-25 amino acids in length, which peptide is covalently attached to the DNA binding domain and does not correspond to a fragment of a naturally-occurring transcriptional activator.
2. The transcriptional activator of claim 1, wherein the peptide is approximately 8-17 amino acids in length.
3. The transcriptional activator of claim 2, wherein the peptide is 6, 8, 11, or 13 amino acids in length.
4. A transcriptional activator comprising:  
a DNA binding moiety; and  
a substantially hydrophobic polypeptide between about 6 and 25 amino acids in length, which peptide is linked to the DNA binding moiety in a manner that does not interfere with its DNA binding activity,  
the transcriptional activator being characterized by an ability, when expressed in yeast cells, to activate transcription from a promoter including a recognition site for the DNA binding moiety approximately 250-1000 basepairs upstream of the transcription start site.
5. The transcriptional activator of claim 4, which transcriptional activator, when expressed in yeast, does not squelch transcriptional activation by LexA-Gal4.

6. The transcriptional activator of claim 5, which transcriptional activator, when expressed in yeast, does not squelch transcriptional activation by LexA-Gal11.
7. The transcriptional activator of claim 4 or claim 5, in which the DNA binding moiety comprises Gal4(1-100) and the activator, when expressed in yeast, activates transcription at least half as well as does Gal4 from a promoter containing at least one Gal4 DNA binding site approximately 250-1000 basepairs upstream of the transcription start site.
8. The transcriptional activator of claim 1 or claim 4 wherein the peptide includes at least one aromatic amino acid.
9. The transcriptional activator of claim 1 or claim 4, wherein the peptide does not include any basic amino acids.
10. The transcriptional activator of claim 1 and claim 4, wherein the peptide is selected from the group consisting of LS4 (QLPPWL; SEQ ID NO: 8); LS8 (QFLDAL; SEQ ID NO: 16 ); LS11 (LDSFYV; SEQ ID NO: 21); LS12 (PPPPWP; SEQ ID NO: 23); LS17 (SWFDVE; SEQ ID NO: 33); LS19 (QLPDLF; SEQ ID NO: 37); LS20 (PLPDLF; SEQ ID NO: 39); LS21 (FESDDI; SEQ ID NO: 41); LS24 (QYDLFP; SEQ ID NO: 45); LS25 (LPDLIL; SEQ ID NO: 47); LS30 (LPDFDP; SEQ ID NO: 55); LS35 (LFPYSL; SEQ ID NO: 57); LS51 (FDPFNQ; SEQ ID NO: 71); LS64 (DFDVLL; SEQ ID NO: 85); LS102 (HPPPI; SEQ ID NO: 92); LS105 (LPGCF; SEQ ID NO: 95); LS106 (QYDLFD; SEQ ID NO: 97); LS120 (YPPPPF; SEQ ID NO: 115); LS123 (PLPPFL; SEQ ID NO: 118); LS135 (LPPPWL; SEQ ID NO: 136); LS136 (VWPPAV; SEQ ID NO: 138); LS152 (DPPWYL; SEQ ID NO: 154); LS153 (LY; SEQ ID NO: 156); LS158 (FDPFGL; SEQ ID NO: 160); LS160 (PPSVNL; SEQ ID NO: 162); LS201 (YLLPTCIP; SEQ ID NO: 167); LS202 (LQVHNST; SEQ ID NO: 169); LS203 (VLDFTPL; SEQ ID NO: 171); LS206 (HHAFYEIP; SEQ ID NO: 175); LS212 (PWYPTPYL; SEQ ID NO: 183); LS223 (YLLPFLPY; SEQ ID NO: 195); LS225 (YFLPLLST; SEQ ID NO: 199);

LS232 (FSPTFWAF; SEQ ID NO: 209); LS241 (LIMNWPTY; SEQ ID NO: 221), each of these peptides extended by Gal4 residues 96-100, and each of these peptides extended by residues corresponding to Gal4 96-100 except that one or both of Gal4 residues 99 and 100 has been substituted with a different amino acid.

11. A method of identifying novel transcriptional activators, the method comprising steps of:

- providing a collection of synthetic oligonucleotides of random sequence, which oligonucleotides are approximately 18-24 base pairs in length;

- linking oligonucleotides from the collection to a nucleic acid encoding a polypeptide with DNA binding activity, thereby producing a library of artificial transcriptional activator genes;

- expressing encoded hybrid proteins from the library of artificial transcriptional activator genes; and

- identifying hybrid proteins that activate transcription.

12. The method of claim 11 further comprising a step of identifying hybrid proteins that, when expressed in yeast cells, do not squelch transcriptional activation by Gal4.

13. A method of activating transcription in a cell, the method comprising:

- providing to the cell a transcriptional activator of claim 1 or claim 4 under conditions that the transcriptional activator will bind to a DNA site in the cell and activate transcription; and

- identifying those transcriptional activators that:

- i) stimulate transcription at least half as effectively as does a known transcriptional activator linked to the same DNA binding moiety and assayed on the same reporter gene; and

- ii) do not squelch transcriptional activation by acidic activators in yeast.

14. In a di-hybrid protein-protein interaction assay the improvement that comprises utilizing Gal11 as a transcriptional activation domain.
15. A method of identifying protein-protein interactions, the method comprising:
  - providing a first fusion comprising a DNA binding domain fused to a library of DNA fragments;
  - providing a second fusion comprising a target protein fused to a polypeptide comprising a region of Gal4 with which Gal11P interacts;
  - introducing the first and second fusion in a cell including Gal11P; and
  - identifying library members that interact with the target protein by identifying those cells in which transcription is activated.
16. An isolated protein that is a derivative of TBP, which derivative is selected from the group consisting of TBP N69R and TBP V71R.
17. A method of altering transcriptional activation, comprising:
  - introducing into a cell a TBP derivative selected from the group consisting of TBP N69R and TBP V71R.